

10/501,566

Sequence Alignments

RESULT 1

US-08-176-126B-2

; Sequence 2, Application US/08176126B

; Patent No. 5589358

; GENERAL INFORMATION:

; APPLICANT: Dawson, Paul A.

; TITLE OF INVENTION: ILEAL BILE ACID TRANSPORTER COMPOSITIONS AND

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: US

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/176,126B

; FILING DATE: 29-DEC-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Parker, David L.

; REGISTRATION NUMBER: 32,165

; REFERENCE/DOCKET NUMBER: WAKE:002/PAR

; TELECOMMUNICATION INFORMATION:

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; TELEX: na

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 348 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-176-126B-2

Query Match 44.7%; Score 884; DB 1; Length 348;

Best Local Similarity 46.9%; Pred. No. 8.9e-82;

Matches 164; Conservative 74; Mismatches 102; Indels 10; Gaps 4;

Qy 7 SSSACPANSS--EEELPVGLEVHGN--LELVFTTVVSTVMMGLLMFSLGCSVEIRKLWSHI 62
:|| | |: : | : | : | :| : | |::: |:|:|:|:|:| | |:

Db 3 NSSICNPNAICEGDSIAPESNFNAILSVVMSTVLTILLALVMFMSMGCNVELHKFLGHL 62

Qy 63 RRPWGIAVGLLCQFGLMPFTAYLLAISFSLKPVQAI AVLIMGCCPGGTISNIFTFWVDGD 122
||||| || ||||:| | :||::| : |||| | | ||||| || | :|||

Db 63 RRPWGI VVGFLCQFGIMPLTGFVLSVAFGILPVQAVVLIQGCCPGGTASNILAYWVDGD 122

Qy	123	MDLSISMTTCSTVAALGMMPLCIYLYTWSWSLQQNLTIPTYQNIGITLVCLTIPVAFGVYV	182
		: : ::: : : : : :	
Db	123	MDLSVSMTTCSTLLALGMMPLCLFIYTKMWVDSGTIVIPYDSIGTSLVALVIPVSIQMYV	182
Qy	183	NYRWPKQSKIILKIGAVVGGVLLLVAAGVVLAKGSWNSDITLLTISFIFPLIGHVTGF	242
		:: ::: :: :::: : : : : : : :	
Db	183	NHKWPQKAKIILKIGSIAGAILIVLIAVVGILYQSAWTIEPKLWIIGTIYPIAGYGLGF	242
Qy	243	LLALFTHQSWQRCRTISLETGAQNIQMCITMLQLSFTAHLVQMLSFPPLAYGLFQLIDGF	302
		: : : : : : : : : :	
Db	243	FLARIAGQPWYRCRTVALETGLQNTQLCSTIVQLSFSPEDLNLVFTFPLIYSIFQIAFAA	302
Qy	303	LIVAAYQTYKRRLKNKHGKKNKSGCTEVCHTRKS--TSSRETNAFLEVNEE	350
		::: : : : : : : :	
Db	303	ILLGAYVAYKK----CHGKNNTLQEKTDNEMEPRSSFOETNKGFPDEK	348

Db

361 MDCHRALEPVGHITSCE 377